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Selection Aspects of Improving the Gene Pool of Dairy Cattle: A case study of Red Steppe Cattle Bred in the Omsk Region

Irina Ivanova[1], Elena Yurchenko[1], Yulia Okoneshnikova[1], Alexey Aleshkov[2], Yulia Diner[1], Natalia Yurk[1] and Olzhas Shoykin[1*]

[1]P.A. Stolypin Omsk State Agrarian University, Omsk, Russia; [2]Pacific National University, Khabarovsk, Russia.
[*]Corresponding author's e-mail: olzhas.shoykin@mail.ru

In the context of globalization, preserving the gene pool of domestic milk cattle is critical for sustainable agriculture in Russia. The Red Steppe breed, traditionally predominant in the Omsk Region, faces competition with the high-yielding Holstein breed. This competition requires the strategic enhancement of the Red Steppe breed's genetic traits to maintain biodiversity and improve milk yield under local environmental conditions. The study focuses on developing a scientifically grounded breeding system to preserve the genetic potential of the Red Steppe breed. The study was conducted on 1,030 cows in the Azovskoe JSC in 2024. Genetic potential was analyzed using parent indices and genotyping on a sample of 50 cows selected based on their parentage. In addition to 2019-2024 productivity data, the study analyzed genetic profiles for marker genes determining milk yield and nutritional composition. Cows with a higher genotype effectiveness index produced significantly more milk compared to those with lower indices. Red Steppe cows showed substantial genetic potential and the leading groups surpassed herd averages by 14.39%. The increased frequency of favorable marker alleles, particularly those associated with milk yield (e.g., CSN2, GHR, ABCG2), was linked to enhanced milk productivity, but also correlated with a higher incidence of reproductive and limb diseases, indicating a trade-off between improved production traits and animal health.
Keywords: Cattle breeds, breeding systems, milk yield, crossbreeding, genetic potential, marker-assisted selection, phenotype.

INTRODUCTION

Improving and preserving the gene pool of milk cattle breeds is a national priority in Russian agriculture. However, amid the globalization of agriculture, many local milk cattle breeds are being forced out of breeding systems due to their inferior competitiveness compared to the leader in milk yield - the Holstein breed. For 70 years, the Red Steppe breed has been the planned breed of dairy cattle in the Omsk Region, as it has successfully adapted to the sharp continental climate of the south of West Siberia and the low nutritional value of local fodder resources. Traditional breeding systems for the Red Steppe breed aim at improving milk yields through accumulation crossbreeding with the Holstein breed (Abylkasymov et al., 2020; Van Schyndel et al., 2019). Over the past two decades, the number of purebred Red Steppe cattle has declined by more than 40%, primarily due to crossbreeding practices aimed at increasing milk productivity (Panfilova et al., 2021).Thus, most herds in the Omsk Region have now transformed the Red Steppe parent material into Holstein highbred. The Red Steppe cattle breed exhibits a unique combination of genetic traits. It has been known to possess high adaptability to hot climate conditions, good enough milk production, and good reproductive function (Suyunova et al., 2024). Recent studies have shown that the Red Steppe breed, though characterized by poor productivity, has incredible resistance to diseases and a robust immune system (Panfilova et al., 2021). In an era of climatic instability and increased stress among global livestock systems, the genetic portfolio of the Red Steppe breed offers valuable resources for future breeding programs. The inclusion of these adaptive characteristics into crossbreeding programs or genomic selection tools enables researchers to enhance the resilience of widely favored breeds without sacrificing levels of productivity.

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Thus, the genetic resilience demonstrated by the Red Steppe breed holds great promise for enhancing the sustainability of cattle production in the face of environmental uncertainty and shifting climatic patterns (Mahdabi et al., 2025).

The realities of economic sanctions call for a global reimagining of the selection strategy in Russian dairy farming. The key strategic priority in securing the import independence of domestic cattle breeding as defined by the President of the Russian Federation is to ensure progress in selection by improving the gene pool of domestic breeds. Economic sanctions imposed on Russia were believed to significantly impact the country's ability to access high-quality genetic material, advanced breeding technologies, and veterinary pharmaceuticals from international markets, but recent studies have shown the contrary positive results (Golovin et al., 2022). This positive outcome is due to the strengthening of local efforts in livestock breeding. The Red Steppe breed, with its proven adaptability, stable milk productivity, and resilience to environmental stressors, serves as a valuable genetic resource for achieving import independence (Panfilova et al., 2021). The government's support for genetic research, local breeding centers, and data-driven selection strategies will be crucial in mitigating the long-term effects of sanctions. Also, the implementation of interest rate subsidies and capital cost subsidies, like during the 2014-2017 counter-sanctions, can go a long way in financing local efforts (Kotyrlo & Zaytsev, 2023). To this end, import independence requires efforts from both the political and scientific spheres of the federation.

Genomic selection techniques shorten the time needed to evaluate animals, determine or validate their origin, and forecast their reproductive and illness resistance. They improve breeding, increase its precision, and drastically shorten the time between generations (Ulimbashev, 2024). In recent years, DNA-based marker technology has identified quantitative trait loci (QTLs) that contribute to complicated variables like milk yield. Using identified QTLs in genetic evaluation can enhance selection accuracy and speed genetic improvement in animal productivity, unlike traditional breeding methods that rely primarily on phenotypic and pedigree information.

Advances in population genetics and genomic technologies enable the optimization of breeding programs and the identification of valuable genetic resources within the gene pool (Roche et al., 2020). Genomic selection has been instrumental in Red Steppe breeding. Ulimbashev (2024) emphasized that to boost production and the expression of the dairy type while maintaining the innate adaptation traits, the current goal of the Omsk breeding effort involved the targeted enrichment of the red steppe cattle gene pool utilizing the related red Danish and Red-and-White Holstein cattle. Hu et al. (2023) highlighted that the genetic diversity of the Chinese Red Steppe primarily focused on the genetic features that contributed to muscle growth and differentiation, milk production, and lipid metabolism. Mahdabi et al. (2025) reported that integrating genomic selection, particularly genomic estimated breeding values (GEBVs), can expedite genetic gains by allowing for the exact identification and transmission of superior alleles associated with critical traits. These tactics, which include deliberate crossbreeding, diligent inbreeding management, and modern genomic technologies, will work together to promote long-term, high-performing cattle populations capable of prospering in adverse conditions while satisfying demand for efficient, ethical beef production. Although comprehensive, their study failed to highlight the phenotypical roles. Sizova et al. (2025), unlike recent studies, utilized a phenotypic approach in determining milk yield by analyzing the effects of housing systems on Red Steppe dairy cows. Sattarov et al. (2022) also took a phenotypical angle in their study on the effect of lightweight housing when raising red steppe in hot climates. They concluded that there was an increase in productivity and natural resilience. These studies highlight that for optimal breeding of red steppe and to maintain their natural desirable traits, it is imperative to consider both genetic and phenotypic factors.

The scientific novelty of the present research lies in a comprehensive characterization of the phenotypes and genotypes of the Red Steppe breed bred in the Omsk Region and the developed system of monitoring for each production cycle stage to assess the quality of the parent material used in reproducing cattle herds. Unlike conventional systems that focus primarily on genotypical factors, biomarkers, and often rely on sporadic evaluations or focus narrowly on milk yield alone, this system utilizes a large sample size, implements historical genetic data from multiple generations, real-time phenotypic assessment and molecular-genetic diagnostics to develop an effective monitoring system adaptable to other cattle breeds.

The study aimed to develop a scientifically grounded selection system to improve and preserve the gene pool of the Red Steppe breed.

MATERIALS AND METHODS

The research was conducted according to the European Convention for the Protection of Vertebrate Animals used for Experimental and other Scientific Purposes (ETS No. 123, Strasbourg, 1986) (Council of Europe, 1986) and Order of the Ministry of Health and Social Development of the Russian Federation No. 708n of August 28, 2010 (Ministry of Health and Social Development of the Russian Federation, 2010).

The studies were conducted at the breeding plant of the Azovskoe JSC, Azovsky Nemetsky National District, Omsk Region in 2024.

The total number of cows involved in the study was 1,030 heads. The genetic potential of milk productivity was analyzed based on the parent index of ancestors influencing the gene pool of the population:

$$PI=(2*M+MM+FM)/4 \quad (1)$$

where: M — productivity of the mother; MM — productivity of the mother's mother; FM — productivity of the father's mother.

Trends in the productive qualities of cows were analyzed using the plant's production reports for 2019-2024.

Out of the total population of cows (n=1,030 heads), based on an analysis of parentage and thorough-bredness by the Red Steppe breed, 50 heads with up to 50% thorough-bredness were selected for the genotyping sample. The genotypes of cows were tested in the Ksistest laboratory, Ksiveliu LLC, Moscow. Biological material in the form of plucked hair samples from live cows was delivered to the laboratory to determine seven genetic productivity markers (CSN2; CSN3; LGB; ABCG2; GHR; GH1_2141; GH1_2291) and 17 genetic anomalies (AX; BY; HY_ERCC6L; HY_TSR2; HH1; HH3; HH4; HH5; HH6; HH7; FXID; BLAD; DUMPS; BDCMP; CVM; MPS_IIB; HCD; CT).

Cows' genotype effectiveness index determined based on genetic testing and the analysis of the animal's genetic profile was calculated as the ratio of the sum probability of the desirable alleles of DNA markers being transferred to the offspring to the reference genotype:

$$Eg=\sum[P_{g1} + P_{g2} + ...P_{gi}]/\sum[G_1 + G_2 + ...G_i] \quad (2)$$

where: P_{g1}, P_{g2}, P_{gi} — the probability of passing on the desired allele of the marker$_1$, marker$_2$, and marker$_i$ gene to offspring; G_1, G_2, G_i — associated genotype of DNA markers 1, 2, and i for productivity traits.

Statistical data processing involved multivariate analysis of variance performed in Microsoft Excel 2013 using the parameters of arithmetic mean, standard deviation, median, Pearson's chi-squared test, and the level of polymorphism according to Robertson.

RESULTS

The research concludes that the cow population is influenced by the genetic potential of breeding bulls (Amerkhanov, 2017). The targeted selection of bulls and their assignment to the breeding stock ensures continuous transmission of hereditary information through generations (Miglior et al., 2005). The bulls assigned to a milk cattle herd belong to the primary Holstein lines. However, Angeln bulls are also occasionally found in the pedigrees. Table 1 shows the genetic potential of the assigned and used breeding bulls based on the parent index.

The assigned breeding bulls are distinguished by high genetic milk yield potential. The plant's population of Red Steppe cows includes a great variety of lines. However, all bulls have high genetic potential in the main milk productivity parameters. The milk yield potential of bulls of the Pabst Governor 889233 line exceeds 15 thousand kg and is combined with a relatively high milk butterfat and protein content. The plant's Cavalier 1620273 line has the lowest milk yield potential of 12,988 kg with a high milk protein potential reaching 3.99%.

Table 1. Parent indices of bulls contributing to the gene pool of the Red Steppe breed in the Omsk region.

Bull line	Parent index		
	Milk yield, kg	Milk butterfat, %	Milk protein, %
Vis Back Ideal 1013415	14,752±477.1	3.98±0.21	3.78±0.16
Montwick Chieftain 95679	13,624±541.1	3.99±0.17	3.83±0.19
Reflection Sovereign 198998	14,255±498.3	3.86±0.21	3.94±0.26
Kvarnakra 22110	14,363±465.8	4.01±0.24	3.95±0.18
Cavalier 1620273	12,988±524.6	4.12±0.16	3.99±0.15
Nokan Olpi 90012	13,856±473.1	4.04±0.18	4.01±0.28
Banko 19665	14,966±518.2	4.20±0.19	3.75±0.18
Pabst Governor 889233	15,427±579.0	4.18±0.26	3.84±0.19
Star 20135	14,272±426.1	3.99±0.17	3.77±0.23
By breed	14,278±498.4	4.04±0.21	3.87±0.20

The bulls used to improve Red Steppe cows belong to the main Holstein lines, including Vis Back Ideal 1013415, Montwick Chieftain 95679, and Reflection Sovereign 198998. The genetic potential of bulls from the leading Holstein lines is within the range of 13,624-14,752 kg of milk, 3.86-3.99% milk butterfat content, and 3.78-3.94% milk protein content. Bulls of the Angler breed are not inferior to the representatives of the main Holstein lines in their productive qualities in milk productivity.

Red Steppe cows have relatively high genetic potential in terms of milk yield. The parent index of cows in the leading group exceeds the potential of the main herd by 1,360.73 kg, or 14.39% ($p<0.01$) (Table 2).

Table 2. Parent indices of cows.

Indicator	Main herd cows	Leading group cows	Cows selected for genotyping
Milk yield, kg	9,453.2±594.3	10,814.3±533.1	7,952.1±342.6
Milk butterfat, %	4.26±0.17	3.97±0.14	4.42±0.16
Milk protein, %	3.69±0.18	3.78±0.22	3.85±0.20

The parent index of milk yield demonstrated by lowbred Holstein cows is lower than the herd average by 1,501.11 kg, or 18.87% ($p<0.01$). The difference between the parent

index of milk yield in cows is selected for genotyping. The difference between the parental milk yield index of cows selected for genotyping and the leading group amounts to 2,862.17 kg, or 26.5% ($p<0.001$). Red Steppe cows with low Holstein parentage are significantly inferior to high-yielding Holsteinized individuals in their parent index but outperform herd averages by 0.16 and 0.17% ($p<0.05$) in the parent mass fraction of milk butterfat and milk protein, respectively. Thus, the cows' parent index suggests high genetic potential in productivity traits.

At any stage of selection and breeding work, be it with a specific herd or an entire population or breed, it is important to understand the economically valuable characteristics of cattle and their genetic and phenotypic manifestations (Halachmi et al., 2008; Hewitt et al., 2020; Konstandoglo et al., 2017). The first step in this process is to analyze the biological activities of the studied population. The biological activities of cattle include a wide range of processes associated with their physiology, behavior, and interaction with the environment. In this interaction with the environment, they display their phenotypic manifestations (Donnik & Shkuratova, 2009; Gorlov et al., 2014; Samburov & Fedorov, 2022).

First and foremost, we studied the cows' milk productivity by analyzing milk yield by lactations and the qualitative parameters of the milk, i.e., the mass fraction of butterfat and protein (Table 3).

Table 3. Cow milk yield dynamics.

Breed	Year				
	2019	2020	2021	2022	2023
Milk yield, kg					
Production report	6,551	7,001	6,808	7,176	7,412
Valuation	6,021	6,235	6,279	7,109	7,395
Milk butterfat, %					
Production report	4.33	4.20	4.20	4.20	3.82
Valuation	4.19	4.18	4.12	4.14	4.18
Milk protein, %					
Production report	3.61	3.54	3.60	3.57	3.52
Valuation	3.38	3.47	3.49	3.52	3.56

Milk yield has shown a positive trend over the past five years. To be exact, the 2023 milk yield amounts to 7,412 kg according to the plant's production reports, which is 861 kg, or 13%, more than in 2019, and to 7,395 kg according to cow valuation, which also exceeds the 2019 level by 1,374 kg, or 22.8%.

The metabolic processes taking place in the cow's body are also reflected by productivity indicators (Galloway et al., 2018; Naumenkova et al., 2023). The nutrients received with feed, such as glucose, proteins, and fats, cover the energy needs of a living organism and pass onto the food obtained from the animal (Barkema et al., 2015; Bijttebier et al., 2017; Borusiewicz & Mazur, 2017). In dairy farming, this applies primarily to the quality composition of milk and its butterfat and protein content.

According to production reports, the mass fraction of butterfat in the milk of Red Steppe cows has declined. From 2019 to 2023, this indicator lowered from 4.33 to 3.82%, by 0.51%. Valuation data, however, are more stable, varying from 4.12 to 4.19%.

Whereas milk butterfat content indicates the energy content of the milk, protein content determines its nutritional value, given that milk protein is the most available protein of animal origin that is almost fully digested by the human body (Sheveleva et al., 2021; Surov et al., 2023). Furthermore, protein content shows how suitable the milk is for cheese production, which refers to its technological properties (Skachkova & Brigida, 2022).

In analyzing the genetic passports of the animals, we compared the factual genotype of the analyzed individual with a reference genetic profile model, which combined the best genotypes with the DNA markers associated with improved milk productivity.

The value of an animal's genotype is determined by homozygosity by productivity marker genes. A homozygote, having two identical alleles, will always, with any selection, pass on the desired allele associated with improved breeding traits to the offspring.

Comparison with a reference genotype demonstrates the extent to which the genotype of the tested individual corresponds to the desired profile (Isupova & Achkasova, 2021; Popov et al., 2020).

Genotype effectiveness is defined by the probability of passing the desired alleles on to the offspring. In the group studied, the variability of the genotype effectiveness index ranged from 0.3 to 0.87. This high variability of the genotype effectiveness index owes to the fact that this criterion was not considered when sampling the cows.

The analysis of cows' productive qualities in connection with genotype effectiveness shows that cows with a genotype effectiveness index above 0.61 are distinguished by high milk yields per lactation (Table 4).

Table 4. Productivity of cows depends on the effectiveness of the genotype.

Indicator	Genotype effectiveness index		
	0-0.4	0.41-0.60	0.61-1.00
Milk yield, kg	4,904±367	7,139±241	7,833±189
Mass fraction of milk fat, %	4.32±0.012	3.98±0.018	3.84±0.016
Mass fraction of milk protein, %	3.21±0.013	3.49±0.016	3.65±0.011

Cows with a high genotype effectiveness index outperformed cows with a low index by 2,928.74 kg, or 59.71% ($p<0.01$), and cows with an average index by 694.7 kg, or 9.73%.

Thus, cows with an index higher than 0.61 can be considered to have the best genotypes that are very likely to pass on the desired alleles of productivity marker genes. The value of cows' genotypes determined based on the genotype effectiveness index can be considered when forming the leading group of the herd.

To summarize, Red Steppe cows possess the genetic resources necessary to improve milk productivity indicators, particularly butterfat and protein content. Some individuals show high indicators across all milk productivity parameters.

On the downside, cows with outstanding genetic qualities can be more susceptible to certain diseases, such as osteoporosis or metabolic disorders (Dunin et al., 2024; Sedykh et al., 2023). For this reason, we also investigated the relationship between cows' genotype and health.

The carriers of genetic cargo can significantly reduce the rate of breeding progress, which makes it important to identify such individuals and adjust selection programs to prevent the spread of genetic anomalies. The group of cows used in our study had no carriers of the genetic anomalies of cattle.

In Table 5, we provide cow incidence rates in relation to the genotype effectiveness index.

Table 5. Cow incidence rate depending on the genotype effectiveness index, %.

Genotype effectiveness index	Gynecological diseases	Diseases of the extremities
0.25-0.40	6	13
0.41-0.60	12	10
0.60-1.00	25	17

An increase in the number of alleles of milk productivity markers in genotypes is associated with a higher incidence of diseases, gynecological and of extremities. Among cows with the share of desirable alleles in the genotype reaching more than 0.6, diseases associated with reproductive dysfunction were more frequent (25%). Although the correction of reproductive qualities is more closely tied to changes in paratypic factors, hereditary determination is still present.

The system of monitoring genetic polymorphism at all stages in the production cycle shapes the quality of the material used to reproduce dairy cattle herds. This system relies on genetic testing and controlling phenotypical indicators. Among the parameters included in this monitoring is the presence of marker genes corresponding to milk yield, butterfat and protein content, and genetic anomalies.

Figure 1. depicts the scheme of monitoring the stages of the production cycle of assessing the quality of reproduction material.

The milk production cycle is composed of key production steps and control points, which follow a specific sequence in the settings of dairy plants.

At the beginning stage of introducing the selection process to improve the Red Steppe breed, the existing cow population is evaluated based on a set of traits (phenotype assessment according to individual and parental productivity). As a result of this evaluation, the conclusion is drawn on the expediency of using the cows in further reproduction. If the cow's results correspond to the goals of selection, a sample of its genetic material is taken for genotyping. The next stage is to calculate and evaluate the genotype effectiveness index. The cows rated as the best are then transferred into the leading group.

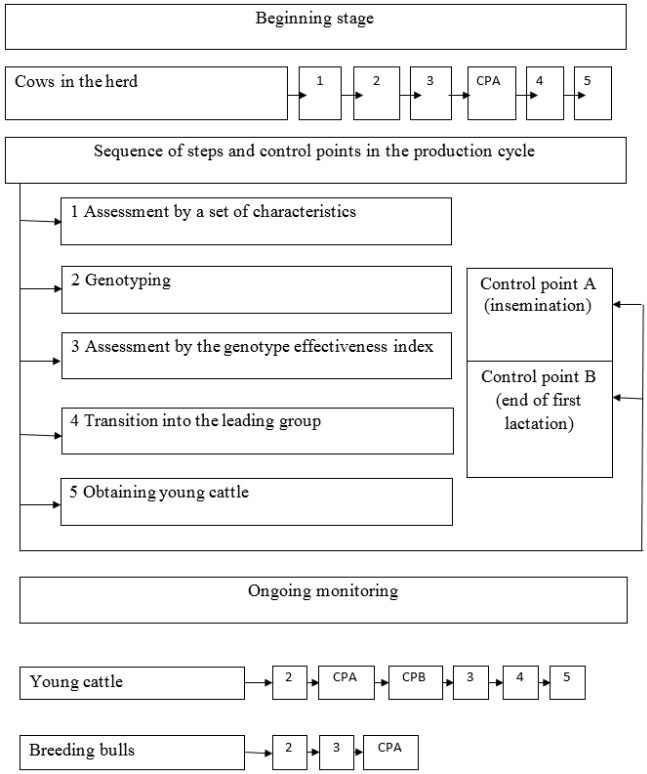

Figure 1. Scheme of monitoring by production cycle stages to assess the quality of the material used in reproduction.

Insemination is a control point in the production cycle that requires particular attention. This is the point at which all the material participating in reproduction comes together.

The ongoing monitoring of the material included in reproduction is cyclical. The start of monitoring is marked by the genotyping of young cattle and a preliminary assessment of the group's correspondence to selection goals. If the preliminary assessment of young cattle based on genetic passports delivers a positive verdict, heifers are

transferred into rearing stock, which then moves on to control point A (insemination) and control point B (end of first lactation). After control point B, the individuals undergo a final assessment, which results in forming the leading group and obtaining young cattle.

To improve the effectiveness of selection, breeding bulls also need to be covered by the monitoring system. After all, the genotype of the breeding bull and its effectiveness are important to test and consider in the selection process.

DICUSSION

Milk is essential for the human body, both in its raw form and as processed products. Throughout history, milk has been the primary source of sustenance. It contains almost 100 different useful nutrients, including fatty acids, amino acids, milk sugar, vitamins, and minerals. Cow milk is one of the most consumed types of milk globally, and in that sense, optimizing milk production is essential in improving various areas of life. The high genetic potential of Red Steppe Cattle displayed in this study suggests that it is an ideal candidate for sustainable dairy systems, especially in subsistence agricultural practices or in regions with limited access to high-quality feed and veterinary support (Khamzina et al., 2024). The herd integration of bulls with high milk productivity genetic potential creates a predictive model to determine what alleles will be passed on to the offspring. This aligns with the studies of Fedorovych et al. (2023a) and Dankiv et al. (2022), who recorded similar instances. The findings of this study prove that the Red Steppe cattle breed possesses genetic potential to improve milk productivity while maintaining its natural resilience to climatic conditions in the Omsk Region. The study demonstrates that by integrating genotype potential with phenotypic performance data, we observe that Red Steppe cows with higher genotype scores significantly outperform their counterparts in milk yield. These findings align with the studies of Suyunova et al. (2024) and Fedorovych et al. (2023b). The observed principle of biological trade-offs marked by an increase in disease susceptibility between cows of higher genetic potential reflects a crucial challenge in modern cattle breeding and genomic selection. This aligns with the studies of Uskenov et al. (2023) and Gadige et al. (2024), who observed similar conditions in dairy cows with increased productivity. Further studies and actions are required in establishing a balance between productivity and health indicators. A limitation faced by this study lies in the relatively small genotyped (n=50) subset despite its large sample size of over 1000. Future research could boost statistical power and provide more in-depth understanding of breed-wide trends and allele distribution by enlarging this sample. Furthermore, as the results showed, health issues were not completely absent from high-performing genotypes. Future breeding initiatives ought to think about utilizing CRISPR-based genomic editing or incorporating disease-resistance markers, two technologies that are being investigated more and more in post-2023 cattle genomics research (Hasan et al., 2022; Liu et al., 2024).

Finally, while this study focused predominantly on maternal lines, future research could expand to include more comprehensive paternal genotype evaluations. Such efforts would enhance the predictive scope of breeding indices and potentially unlock even higher productivity and adaptability in composite Red Steppe populations.

All things considered, in the age of sustainable, resilient agriculture, the Red Steppe breed - long eclipsed by global Holstein supremacy - is becoming increasingly important as a genetic source. Marking significant progress in regional dairy genetics, the present work offers a fresh approach combining multi-generational data, genotype effectiveness indexing, and phenotypic evaluation. These results support more general projects to guarantee the long-term survival of Russia's dairy industry, increase import independence, and strengthen domestic breeding programs.

***Conclusion*:** The study draws attention to the genetic potential of the Red Steppe cattle breed as a foundation for raising milk productivity while preserving adaptability to the challenging environmental conditions of the Omsk Region, Russia. The findings broaden the scientific understanding of important aspects in selecting gene pool cattle breeds and shed light on potential opportunities to boost the effectiveness of breeding the Red Steppe breed in the region. The results show that cows with a higher genotype effectiveness index significantly outperformed their peers, achieving up to 59.71% greater milk yields. However, the association of highly effective genotypes with increased susceptibility to diseases emphasizes the need for comprehensive approaches to selection and health management. Future research should focus on optimizing genetic markers to balance productivity and resistance. Predictive models aimed at minimizing genetic disorders while enhancing desired traits can greatly advance selection programs. A promising direction for the improvement of selection strategies is to integrate genomic tools with traditional phenotypic evaluations. Furthermore, researchers should explore the potential of crossbreeding to combine the endurance of the Red Steppe breed with the productivity characteristics of Holstein lines while ensuring genetic diversity and resistance.

***CRediT author statement*:** Irina Ivanova and Elena Yurchenko contributed to the conceptualization and design of the study. Yulia Okoneshnikova and Alexey Aleshkov performed data collection and laboratory analysis. Yulia Diner and Natalia Yurk carried out statistical analysis and interpretation of the results. Olzhas Shoykin supervised the

research process, provided project administration, and served as the corresponding author. All authors contributed to manuscript drafting, critically reviewed the final version, and approved it for submission.

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***Availability of data and material*:** The datasets generated and analyzed during the current study are available from the corresponding author upon reasonable request

***Consent for publication*:** Not applicable

***SDGs addressed*:** Zero Hunger, Responsible Consumption and Production, Climate Action.

***Policy referred*:** National Policy on Genetic Resource Preservation

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